scRNAseq analysis

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07/14/2023

import numpy as np  
import pandas as pd  
import scanpy as sc  
import scipy  
import os  
import scipy.io as sio  
  
data\_path = "Z:/ResearchHome/Groups/sapkogrp/projects/RNAseq/common/scRNAseq\_Paul\_cardiomyopathy/newvolume/analysis/S\_combined/all-well/DGE\_filtered/"

# Adjusting scanpy default settings

Scanpy allows you to customize various aspects of the default package behavior.

sc.settings.verbosity = 1 # verbosity: errors (0), warnings (1), info (2), hints (3)  
sc.settings.set\_figure\_params(dpi=100, fontsize=10, dpi\_save=300, figsize=(5,4), format='png')  
sc.settings.figdir = 'Z:/ResearchHome/Groups/sapkogrp/projects/RNAseq/common/scRNAseq\_Paul\_cardiomyopathy/newvolume/analysis/combined\_figures/'